Gendore vorsion 4 5 Copyright (c) 1993 - 2000 compugen Ltd

OM protein - protein search, using sw model

April 24, 2002, 10:37:58; Search time 71.56 Seconds Run on:

(without alignments) 82.491 Million cell updates/sec

US-09-525-998A-2_COPY_11_201 941 1 DSVCPQGKYTHPQNNSICCT..... Fitle: Perfect score: Sequence:

....CSNCKKSLECTKLCLPQIEN 161

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched!

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2ոննդնոնն

Post-processing: Minimum Match 1008 Maximum Match 1008 Listing lirst 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	SOMETHE STATES	Description	TNR1_HUMAN P19438 homo sapien	P1G P50555 sus s	- T.	2		AN	P36941	P08138	ш Som 911251			982220		C140_MCUSE		028203 bos		P34015	ы	1,20333	061260	118519	956760	_DPOME	F41272	HUMAN	HUMAN 126842	. 09nj15	MUDSE OUT OUT	P92127	DON'T HIMAN
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"Two tumor necrosis Lactor-binding proteins puritied from human urine. Evidence for immunojaical cross reactivity with rell surface tumor necrosis factor receptors.";
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Bannor D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,
Broger C., Loetscher H., Lesslauer W. "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
Pera complex: implications for TNF receptor activation.";
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DOMARN THE DOMAIN THAT INDUCES A SAMASE IS FREGABLY IDENTICAL TO
THE DEATH DOMAIN. THE N. SMASE ACTIVATION DOMAIN (NSD) IS BOTH
NECESSARY AND SUFFICIENT FOR ACTIVATION OF N.-SMASE.
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"Structures of the extraoglidat domain of the type I tunor necrosis
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                                                                                                                                                                                                                                                                                                                                                                                                Fuchs P., Strehl S., Dworzak M., Himmler A., Ambros P F; "Structure of the human TNF receptor 1 (p60) gene (INFR1) and localization to chromosome 12p13.";
expression of recombinant soluble INF-binding protein.", Proc. Natl. Acad. Sci. II. S. A. R7-7786-7784 (1990)
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MEDLINE-97094982; PUDMEd-8939750;
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AAA36756.1;
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EMBL; M33294: AAA04210 1: -
EMBL; M58286; AAA36753.1; -.
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TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MISSING (IN REF. 4).
GPAA -> APP (IN REF. 4).
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INFR-CYS 4.
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                                                                                                                                                  PPOSITE; PS50050; INFP_NGFR_2; 3.
PROSITE; PS50017; DEATH_DOMAIN; 1.
                                                                                                                                          PROSITE: PS00652; TNFR_NGFR_1; 3.
PPOSITE: PS50050; TNFR_NGFR_2; 3.
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                                                                                                               PD000771; TNFR_c6; 1.
                                                                                       'INF'R_C6.
                                                                              interPro; IPR000488; Death.
A21522; CAA01558.1;
A34899; GQHUTI.
                                                                                                       PF00020; TNFR_C6; 4.
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                                                                                               Pfam; PF00531; death; 1.
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SMART; SM00208; TNFR; 4.
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41 DSVCPQGKYTHPQNNSTCCTRCHKGTYLYDDCPGPGQDTDCRECEGSFTASENHLPHCL 100 10) SCSKOBKERGOVEJSSOTVURPTVOGOPKNOYRHYWSENLFQCFNOSLOLNGTVHLSCQE 160 1 DSVCPQGKYTHPQNNSTCCTFCHKGFFLYNDCFCPQDDTDCFECESGSFTASENHTRHCL, 60 100.0%; Score 941; DB 1; Length 455; lin 0%; Pred, No. 5e-71; 0; Indels 12: KONTVOTOHAGEELPENEOVSOSNOKKSLEOTKIOLPQIEN 161 161 KONTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQ1EN 201 0; Mismatches Matches 161; Conservative Local Similarity Query Match 3

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RESULT

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Gence 163-264 266 (1945)

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                                                                           01-0/I-1996 (Rel. 34, Created)
01-0/I-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TUMOR NECHOSIS FACIOP PECEPTOR 1 PRECUESCE (PEG) (TNP P1) (TNP-RI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. SIMILARITY: CONTAINS A LA-NGERZTHER TYPE CYSTEINE-RICH REGION. 1. SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                  Sus scrota (Piq).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria, Cetartiodactyla; Suina, Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSS0017; DEATH_DOMAIN; 1.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TUMOR NECROSIS FACTOR RECEPTOR 1.
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SUBGELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
    PRT; 461 AA
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TNFR-CYS 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Kidney;
MEDLINE-96011645; PubMed-7590278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS00652: TNFR_NGFP_1: 4. PP0SITE: PS50050; TNFP_N0FP_2; ?
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    STANDARD;
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SMART; SM00208; TNFR: 3
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                                                                                                                                                                                                                                                                                               INFRSF1A OR INFR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCB1_Tax1D-9823;
INR1_PIG
P50555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suter B.,
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Mol. Cell. Riol. 11:8020-3026(1991).
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 Eukar_Iota, Metuabou, Chorduta, Craniuta, Verrebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis factor receptor.";
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Gray P.W., Feldmann M., Foxwell B.M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             $1.47 TE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.1%; Scote 716.5; EB 1: identifi 461: 77.4%; Pred. No. 1.7e=5.; (1.5e-7); 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and expression of conAs for two distinct muring tumor
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Lewis M., Tartavila L.A., Lee A., Rennett G.L., Rice G.C.,
Wong G.H., Chen E.Y., Goeddel D.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: Mull. A.ad. Sti. 7.3.A. 88.1840 1941)
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101 PERMEDIA DE HATTELLET EL TELETON PERMENSIONALES PARMES 194
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Best Local Similarity
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SEQUENCE FROM N.A.
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AC P25118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEASES) MEDIATING APOPTOSIS (BY SIMITAPITY)
SUBUNIT: INF BINDING TO THE EXTRACELLULAR DOMAIN OF TNERL LEADS TO
                                                                                              "Molecular cloning and expression of the mouse Inf receptor type b "; Insumogenetics 34:338\cdot340(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTIVALES AT LEAST TWO DISLINCE SEGNALING CASCADES, AFOLTOSIS AND NF-KAPPA H SIGNALING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMOTRIMERIZATION, ONCE ACCREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLFOTLAR INTERPACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF FRADE, VARIOUS TRADE-INTERACTING PROPERIS STRIP AS TERS, FIF AND POSSIBLY FALE, ARE RECOURSED FUNERLY COMPLEX.

    -1 - SURCELLULAR LOCATION: TYPE I MEMPRANE PROTEIN.
    -1 - SIMILARITY: CONTAINS A LA-NGFR/THER-TYPE CYSTEINE-PICH REGION.
    -1 - SIMILARITY: CONTAINS I DEATH DOMAIN.

                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: RECEPTOR FOR TWE ALPHA, THE ADAPTOR MOLECULE FADD
FECRULIS CASPASE-B TO THE ACTIVATED RECEPTOR. THE RESULTING
AGGREGATE CALLED THE DEATH: INDUCING SIGNALING COMPLEX (DISC)
PERFORMS CASPASE'S PROFESTYIC ACTIVATION WHICH INITIATES THE
SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
                                                                                                                                                                                                                                                                                                                                                        "Genomic organization and promoter tunction of the murine tumor
                                                                                                                                                                                                                                                                                                                                     Gentz R., Lesslauer W., Steinmetz M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TUMOR NECROSIS FACTOR PECEPTOR 1.
                                                                                                                                                                       MEDLINE-94245292; PubMed-8188324;
BEDD 9.E., Linthicum D.S.;
"Nucleotide sequence of the INF type I receptor from a mouse
endothelioma cell line.";
                                                       MEDLINE-92039815; PubMed-1657766;
Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                      necrosis factor receptor beta qene.";
Mol. immunol, 30:165-175(1993).
                                                                                                                                                                                                                                                                                                               MEDLINE-93156721; PubMed-8381516;
Rothe J., Bluethmann H., Gentz R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M76656; AAA40465.1; -...
EMBL; M88067; AAA40465.1; JOINED.
EMBL; M76655; AAA40465.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE, PSOO652, TWER_NGER_1; 3. PROSITE; PS50050; TWER_NGER_2; 3. PROSITE; PS50017; DUATH_DGMAIN, 1
                                                                                                                                                                                                                                                     Immunogenetics 39:450-451(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
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EMBL; M59377; AAA40464.1; -.
EMBL; X59238; CAA41922.1; -.
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MGD; MGI:1314884; Intrs(la.
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SMART: SM00208; INFR; 3
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$19021; $19021
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                  SEQUENCE FROM N.A.
                                         18SUE-Spleen;
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N-LINKED (GLUNAC. . . ) (POTENTIAL).
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
THMOR NECFOSIS FACTOR PECEPTOR 1 PRECURSOR (PAG) (INF-R1) (INF-R1)
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Eskuryota, McLuzou; Chorduta, Craniata, Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodaetyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: RECEPTOR FOR THE ALPHA. THE ADAPTOR MOLECULE FADD
RECKLIS CASIASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIALES THE
SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
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"Cloning of cDNA encoding bowine Lumor necrosis factor receptor I
(TNP-RI).";
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                                                                                                                                                                      N-SMASE ACTIVATION DOMAIN (NSD).
DEATH.
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71.3%; Pred. No. 1.7e-49;
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  EXTRACELLULAR (POTENTIAL)
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                                      CYTÓPLASMIC (POTENTIAL).
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Bovidae; Bovinae; Bos.
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DOMAIN
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                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib-ch/announce, or send an email to licensetisb-sib.ch).
            SUBUNIT: THE BINDING TO THE EXTRACELLUIAR DOMAIN OF THEFT LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS HOWOURS A NOVEL MOTEULAR INTERPACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF FRADD. VARIOUS TRADD-INTERACTION FROME FROME FROME THAT INTERACTION THAT IS THAT'S THAT STAFFS. BY AND POSSIBLY PAGED, ARE PEPPHITED TO THERE COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
                                                                                               ACTIVATES AL LEASI INO DISTINCT SIGNALING CASCADES, APOPTOSIS AND WEARAPPA B SIGNALING (HY SIMILARITY).
SUBCELLULAR B TOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS A LA-NGFK/TNPR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein, Repeat, Signal; Apoptosis.
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..) (POTENTIAL).
..) (POTENTIAL).
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N-LINKED (GLCNAC) . . .) (PC
N-LINKED (GLCNAC) . . .) (PC
: 5243EF514DFE81C4 CRC64);
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 PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY)
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TNFR-CYS 3.
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PPOSITE: PSSO050; TNFP_NGFR_2; 2.
PROSITE: PSSO017; DEATH_DOMAIN; 1.
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151
51367 MW:
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                                                                                                                                                                                                                                                                                                                                              InterPro; IPPON1368; TNFP_c6
Pfam: PF00531; death; 1.
                                                                                                                                                                                                                                                                                                   EMBL: U90937: AAB65143.1;
                                                                                                                                                                                                                                                                                                                              InterPro; IPR000488; Death.
                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00020; INFR_G6; 3.
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SMART; SMOO208; INFR; 3.
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471 AA;
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SOSKOPKEMAQVEISSOTVEPETVOOPPRAAVPHYWSENLEGOFNOSLOLNGIVHLSOQE 120
71.7%; Score 674.5; DB 1; Length 471;
71.6%; Pred. No. 5e-49;
Live 17; Mismatches 26; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. DSVCPQGRV THPQNNSTQCTKCHKGTYLYNDCPGPGDDTDCPRCFSGSFTASENHLRHCL, KO
                                                                                                                                                                                                                                                                                                                                                                                                 Matches 111; Conservative
                    Ouery Match
Best Local Similarity
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TUMUR NECROSIS FACTOR RECEPTOR 1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this chalcement is not removed. Usage by and for commercial extilities institutes a literary alternative \{\forall x \in \mathbb{N}^+ \mid x \neq 1\} and it connects or send an email to licenserish ships.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PERFORMS CASIVASE-8 PROJECTIVE ACTIVATION WHICH INITIALISES THE BORDEROUSE TO CASTALS. (ASSEMBLATE SPECIFIE). CYSTEINE PROTEOSES, MEDITATIN APPOPUSIS (BY SIMILIARIES) PROTEOSES. MEDITATIN APPOPUSIS (BY SIMILIARIES) PROTEOSES. SUBBUNIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF THEFT LEADS TO PROGENERATE THE REPETIONES DATH BOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEALH DOMAIN OF TRADD. VARIOUS IRADS-INTERACTING PROTEOSES. SIGH AS TRAPS, RIP AND POSSIBLY PADD. ARE RECEPTIFED TO INFRI COMILEX BY THEIR ASSOCIATION WITH IRADS. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES. APPOPUSES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Himmler A., Maure-Flody I., Kracuke M., Schellen P., Filzenmaier K., Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.:
"Molecular claims and expression of human and fat tumor necrosis actor receptor chain (Pob) and its soluble datrice tumor necrosis necrosis factor blanding profession."

DNA Cell Biol. 9:705-715(1990).

PROCEED REPERTY FOR THE ALPHA. THE ALAPTER MOLECULE FALL REPERTY FOR THE ALAPTER MOLECULE FALL REPERTY FOR THE PROFESSIONS. THE RESULING AGGREGATE CALLED THE DEATH-INDUTING SCOMPLEX (D1SC).
101 SCSROKEFMILVELLHIVVERMIVELHANDYRELM ELLERISLEPNITVIFCUE 160
                                                                                                                                                                                                                                                                                                                                                                                                            Enkaryola, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Kattus
                                                                                                                                                                                                                                                01.AUG-1991 (Bel. 19, Created)
01.AMR-1992 (Fel. 21, Last, sequence update)
20.AUG-2001 (Fel. 40, Last, annotation update)
10MCR NUCKOSIS FACION NECERION I FARCONSON (FOU) (INF-RI) (INF-RI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NE-KAPPA E SIGNALING (BY SIMILARITY).

1 SUBCELLULAR LOCALION: TYPE I MEMBRANE PROTEIN.

1 SIMILARITY: CHAINEA I JAHEN MINEMETTE, CYSTEINE MINEMETTE.

1 SIMILARITY: CHAINEA I DEATH DAMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PSGGGS: INFR_MSFR.1; 4.
PPGSIJE: PSGGGS: INFR_MSFR.2; 4.
PROSITE: PSSGG17: DFALH_NOMAIN; 1.
Receptor: !tansmembrane; S!ycoprofeth; Repeat; Signal: Apoptosis.
                                             121 KONPVCTOBAGEFURENHEVSGSNOKKSLECTKLC 155
                                                                                        1+1 POPTIOHOUMGPELKSARCISCHLORAK-BOEKLG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE 91090841: PabMed 1702294:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterFro. IPRSol3f8, INFR_cf.
Pfam; PF00531; death; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF000Z0; FNFR_c4; 4.
Probom; Pb000771; FNFR_c6; 1.
                                                                                                                                                                                                                                                                                                                                                                   INPRSEIA OR INFR! OR INFR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P19438; IINR.
InterPro; IPR000488; Death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBI.; M63122; AAA42256.1;
                                                                                                                                                                                                         S:ANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMARI; SMODOOS; DEATH: 1
SMARI; SMODOOB; INFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                             Fartus normequeus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIP: PP6555; HR6555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCB1_1ax1D=10116;
                                                                                                                                                                                                       I'N#1_KAT
                                                                                                                                                                                                                                 P22934;
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01-NOV-1997 (Rel. 35, last sequence update)
20-AUG-2001 (Rel. 40, last annotation update)
WSL-1 PROTEIN PRECURSOR (AFOFFGETS METAIIM: FEREPINE DR3) (APOPTOSIS-MEDIATING RECEPTOR TRAMP) (DEATH DOMAIN RECEPTOR 3) (WSL PROTEIN)
(APOPTOSIS INDUCING PEREPINE AIP) (AFO-3) (IYMPHOTYIE ASSOCIATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kilson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T., Grinham C.J., Brown R., Farrow S.N.;
"A death domain containing receptor that mediates apoptosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    STSKTRKEMGQVEISSTTVFFFTV000TPKNQYPPPWSFNLFQTFNTSLJLNGTVHLSGQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 SCATCHARMAUVELSPERALIMITVEGERANGPORYLSELHFOCVDGSPERNGTVTTPCKE 150
                                                                                                                                                                                                                                                                                                                                                                                                                      1 DSVCPQGKYTHPQNNSTCCTRCHAGTYLYNDOPGPGDTDCRECESGSFTASENHLRHCL, 60
                                                                                                                           PERMILARITY.
BY SIMILARITY.
BY SIMILARITY.
RY SIMILARITY.
RY SIMILARITY.
BY SIMILARITY.
AN INTERPORTATION (GICNAC. . . ) (POTENTIAL).
N.LINKED (GICNAC. . . ) (POTENTIAL).
N.LINKED (GICNAC. . . ) (POTENTIAL).
N.LINFED (GICNAC. . . ) (POTENTIAL).
N.LINFED (GICNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Exteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSEL_BUMAN STANDARD; PRT; 417 AA.
Q93038: Q93036: Q93037: Q92444: P28415; 249831: Q94722: P78507;
                                                                                                       N-SMASE ACTIVATION DOMAIN (NSD).
                                                                                                                                                                                                                                                                                                                                                                      Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapions (Human).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Eutele
Mammalia: Eutheria: Primates: Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MULAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                             Indels
 EXTRACELLULAR (PUTENTIAL).
                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 KONIVCICHAGFFLRENEGVSGSNCKKSLECIKLCLPQIEN 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.18; Score 669; DB 1;
68.38; Pred. No. 1.46-48;
after 18; Mismalohes 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECEPTOR OF DEATH) (LARD).

THERSF12 OR WSLI OR WSL OR AFOR OR DR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 X TINFR-CYS.
                                                    INFR-CYS 1.
                                                               INFR-CYS 2.
INFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Umbilical vein endothellal cells;
                                                                                           TNFR-CYS 4
                                                                                                                     DEATH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T1SSUF-Lymphoid:
MEDLINE-97088617; PubMed-8934525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                              50969 MW:
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 384:372-375(1996).
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1166
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1196
158
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172
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181
99
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143
158
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151
201
461 AA:
                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                 102
105
127
146
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168
182
185
                                     443
1126
1267
367
444
59
628
844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBL_TaxID-9606,
                                                                                                                                           DISULFID
            RANSMEM
                                                                                                                                DISULFID
                                                                                                                                                                       DISHLFID
                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                 DISHIP
                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                   DISHLFID
                                                                                                                                                                                                                                                               DISHIPID
                                                                                                                                                                                                                                                                            DISULPID
                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 098830;
                                                 REPEAT
PEPEAT
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NIVWOO
                       DOMA I N
                                      DOMA I N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See Attp.//www.isb-sib.ch/announce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chaudhary P.M., Hood L.E.;
Submitted (JAN-1997) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: INDUCES ADPTOSIS AND ATTVATES NUCLEAR FACTOR KAPPA-B
-!- FUNCTION: INDUCES APPTOSIS AND ATTAINE MAINTAINE MAY BLAY A ROLE IN REGULATING LYMPHOCYTE HOMEOSTASIS.
-!- SURUNT: HOMODIMER INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH THE THENT HASSOCIATED MOLECULE TRADD AND THE INRET RECEPTOR TO ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 4-017 And Franciscope of the Management of TESUB-Brain, and French lung;
TESUB-Brain, and French 1952839;
MCDELNE-9720533;
Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
Thome M., Hornand T., Hahne M., Schroeter M., Wilson A., French L.E.,
Thome M., Hornand T., Hahne M., Schroeter M., Willson A., French L.E.,
Thome, M., Hornand T., Tschopp, J., Will, Septence composite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBGELLIGAR LOTATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
ALTERNATIVE PRODUCTS: 3 1SOFORMS; WSL-1/IARD-1A (SHOWN HERE),
WSL-2-IJARD-3 AND WSL-32, ARE PRODUCED BY ALTERNATIVE SPLICING;
TISSUE SPECIFICITY: ABUNDANTIX EXPRESSED IN THYMOCYTES AND
LYMPHO-YTES DETECTED IN LYMPHO-YTE-PICH TISSUES SUCH AS THYMUS,
COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.
FIM: GLYCOSYLATED (PROBALE).
SIMILARITY: CONTAINS A LA NGER/FURF-TYPE CYSTEINE-RICH REGION.
SIMILARITY: CONTAINS I DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prowning J. L., Macdonald H.R., Tschopp J.; "TRAMP, a nevel appetusis mediating temperature with segmence homology to tumor necrosis lactor receptor I and Fas(Apo-1/CD95).";
                                                                                                                                                                                                                                                                                                             Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.I., Goddard A.D., Hauer K.D., Ashkenazi A.; Appr.3, a new member of the tumor nectosis fartor receptor tamily, contains a death domain and activates apoptosis and NF-Kappa-B."; Curr. Biol. 6:1669-1676(1996).
                                                                                                                                                     SEQUENCE FROM N.A.
Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;
Submitted (JAN-1997) to the EMBL/GenBank/100BJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "LARD, a new lymploid specific death domain containing receptor regulated by alternative pre mRNA splicing.", Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
                Chinnalyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garq M., Duan D.P., King I., Gentz P., Ni J., Dikit V.M.; "Signal transduction by DR3, a death domain-containing receptor related to TWFR-I and CD95.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screaton G.R., Xu X.-N., Olsen A.L., Cowper A.E., Ian R., MrMichael A.J., Bell J.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license∉ish sib.ch).
                                                                                                                                                                                                                                                                                            MEDLINE-97148200; PubMed-8994832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=97272273; PubMed~9114039;
MEDLINE-97081063; PubMed-8875942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Y09392; CAA70561.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HMBL; Y09392; CAA70559.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHOUFINCE OF 7-417 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U83599; AAB41434.1;
U83600; AAB41435.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U72763; AAC50819.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [mmunity 6:79-88(1997).
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NISSUM-Brain;
                                                                                                                                                                                                                                                                         LISSUE-Heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMB1.;
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VLGPGAPGWPCGPPPAWGHPDLHTPPLLASQAPGYCR (IN
                                                                                                                                                                                                                                                                                                                                                                                         MEWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG
MEALTPPPATHLS -- SPWCAGNAFGFTGMCFGEGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L->A: SUPPRESSES HOMODIMERIZATION, TNFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 GQVE.1887.1VDKD1VGGCRKNQYRHYWSENLFQC----FNGSLGLN-GTVH----LSCQ-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 HPQNNSICCIKCHKGIYLYNDCPGPGPGQDTDCREGESGSFTASENHLR-HCLSCSKCPKEM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 HKKIGLFOTBGCPAGHYLKAPGTEPGGNSTCLVGPGGTFLAWENHHNSEGARGGAGDEGA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNFRI INTERACTION.
D->A: SUPPRESSES HOMODIMERIZATION, AND
TNFRI INTERACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L->A: SUPPRESSES HOMODIMERIZATION, AND
                                                                                                                                                                                                                                                                                                                                               STI.GGCPFPGAAVGGWPQMFWVQVII.AGI VVFLLLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERACTION, AND APOPTOSIS INDUCTION.
                                                                                                                                                                              Receptor; Apoptosis; Alternative splicing; Transmembrane; Signal;
                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                               NHPTPTSCFQCSGSRCSWLALWSPSCLGPP (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.2%; Score 200.5; DB 1; Length 417, 29 8%; Prod No. 5 8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72; Indels
                                                                                                                                                                                                                                                                                                                                                                                MISSING (IN 150PORM WSL-S1)
                                                                                                                                                                                                                                                                                                                                                                                                                       ISOFORM WSL-S2),
MISSING (IN ISOFORM WSL-S2)
                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPR -> AAA (IN REF. 6).
P -> H (IN REF. 7).
P -> L (IN REF. 7).
A -> R (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R -> 1, (IN REF. 1).
R -> H (IN REF. 1).
F 52263190F0446706_CRC64,
                                                                                                                                                                                                                                  POTENTIAL.
CYFOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                    (IS-ISM MHOHOSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48; Conservative 20; Mismatches
                                                                                                                                                                                                              WSL-1 PROTEIN
                                                                                                                                                                                                                                                        4 X TNFR-CYS.
                                                                                                                                                                                                                                                                            TNFR-CYS 2.
INFR-CYS 3.
INFR-CYS 4.
                                                                                                                                                                                                                                                                    INFR-CYS 1
                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                DEATH
                                                                                                                                                                 PROSITE: PS50017; DEATH_DOMAIN; 1.
                                                                                                                                  Pfam; PF00020; INFR_c6; 2.
PROSITE; PS00552; INFR_NGPR_1; 2.
U78029; AAB40918.1;
U44511; AAB3714.1;
U44501; AAC51305.1;
U44504; AAC51309.1;
U73381; AAC51192.1;
U75381; AAC51192.1;
U83597; AAB41432.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45385 MW;
                                                                                                InterPro: IPR000488; Death.
InterPro: IPR001368: TNFP_c6
                                                                                                                                                         PROSILE; PS50050; TNFR NGFR
                                                                                                                                                                                                    24
417
199
                                                                                                                                                                                                                                                                                                                         67
106
218
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                                                                                                                       Piam; PF00531; death:
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312
370
381
417 AA;
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Bost Local Similarity
                                                                            P19438; ITNR.
                                                                                                                                                                                                   255
256
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 EMBL; U78029;
                                                                                       MIM; 603366;
                                                                                                                                                                                                                      DOMAIN
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CARBOHYD
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VARSPLIC
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                                                                                                                                                                                                                                                                                                              MEDLINE-94225209; PubMed-H171423; Crowe P.D., van Arsdale T.L., Waller B.N., Ware C.F., Hession C., Encowe P.D., van Arsdale T.L., Maller B.N., Ware C.F., Hession C., Encentels B., Escentina J.L., Din W.S., Goodwin R.S., Smith C.A.; Alrender-specific receptor."; Science 244:707-710(1994).

Science 244:707-710(1994).
                       01-JNN-1994 (RG), 29, Created)
01-JNN-1994 (RG), 29, Last sequence update)
01-JNN-1994 (RG), 29, Last sequence update)
2.ANO-2000 (RG), 40, Last annotation update)
2.RELATED PROTEIN (TUMOR NECRESTA FACTOR (TRESEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBCELLULAR LYCATION: TYPE I MEMBRANE FROTEIN.
1 SIMILARIIY: GAMARINS A LA-MOTRZINER-IN-PE CYSTEINE RICH PEGION.
                                                                                                                                                                                                            MEDLINE-93252481: PubMod-M486360;
Baens M., Challanet M., Casalman J.J., den Beruhe H., Marynen P.,
Construction and evaluation of a function Thrary of Luman Lzp
Lranscribed sequences derived from a somatic cell hybrid.";
Ocnomics 16:214-218(1993).
                                                                                                           Homo Sapiens (Human).
Erkaryota: Metaroa: Cherdata; Prasiata: Vertebrata: Enteleustomi:
Mammalia: Eutheria: Primates: Catarrhini: Huminidae: Humo.
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N.LINKEL (GLUNAC. ...) (POTENTIAL).
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PROSLIE; PS00652; TNFR_NGFR_1; 2.
PROSLIE; PS50050; TNFR_NGFR_2; 3.
Receptor: fransmenbrane; Glycoprolein; Repeat; Slyndl.
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EXTRAGELLULAR (POLENTIAL)
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INFR TYS 4
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INFR_c6, 1.
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                                                                                                 LIBR OR INFOR OR INFRSE3.
STANDARD;
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Probom: P0000771; INFR_c
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                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                       NCBI_TaxID-9606;
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 TNRC_HUMAN
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                                                                                                                                                                                                                              49 EYYEPOHR ICCSROPPGIYVSAKO-SRIPDIVCAICAENSYNEHWNYLTICQLORPCDP 106
                                                                                                                                                                                                            AR PMGQVETSSOTVIPPITVOGGERNQVPHYWSPNLFQGENGSL++-CLNGTVHLSGQE--KQ 122
                                                                                            13; Caps
                                                                                                                                 8 KYTHPONNSTOPTKOHKSTYTYTNISPIGNISPIGERGESETASENHLIRHCLISCSKORK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-87051725; PubMed-3022937;
Johnson D., Lanahan A., Huck C.P., Sebgal A., Morgan C., Mercer E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1988 (Rel. 08, Last sequence update)
20-AUG-2001 (Pel. 40, Last annotation update)
LOW-AFFINITY NERVE GROWIH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR) (GPR0-LNGFR) (P75 ICD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SUBCELLULAR LACATION: TYPE I MEMBRANE PROTEIN.
-i- PTM: N- AND O-GLYCCSYLATED AND IS PHOSPHORYLATED ON SERTINE.
i- SIMILARITY: CONTAINS A LA-NGER/INFR-TYPE CYSTEINE-RICH REGION.
-i- SIMILARITY: CONTAINS I DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukarycta, Mctazou, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROTCH DISHLFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (o) Cell. Hiol. B.3160-3167(1988).
!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGE, BONE, NT-3, AND NT-4.
                                                      PR 1; Length 435;
                                                                                            71; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bothwell M., Chao M.;
"Expression and structure of the buman NGF receptor ";
Cell 47:545-554(1986).
46709 MW; 62452585022P656P CRC64;
                                                  19 9%; Soure 187 %; DR 1
32.7%; Pred, No. 7 1e-09;
ive 17; Mismatches 71
                                                                                                                                                                                                                                                                                                                                                                                                                            427 AA
                                                                                                                                                                                                                                                                                      123 NTVOT-CHAGFELPENEOVSCSNCKKSLEC 151
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MEDLINE-89096903; PubMed-2850481;
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01-AUG-1988 (Rel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
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                                                                                            49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                    Query Match
Best Local Similarity
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SEQUENCE
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63 SKYPKEMIQVEISS-TTVEPPTVOGTPKNQYPHYWSENLFQCENOSLOLNGT-VHLSOQE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 CPQCKYTHPQNNSTCCTKCHKCTYLYNDCPGPGDDTDCREC-ESGSFTASENHLRHCLSC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 CPTGLYTH - SGECCRACHLCHGVAQPC-GANG TVCHPCLDSVTESDVVSATFECKPC 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                    BO9FA143FB3D625B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-91187885; PubMed-1849278; Lewis M.; Rice G.C., Lewis M., Tarlaqlia L.A., Lee A., Bennett G.L., Rice G.C., Rong G. H., Chen E.Y., Goeddel D.V., "Cloning and expression of cDNAs for two distinct murine tumor
                                                                                                            LOW-AFFINITY NERVE GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 427;
                                  PROSITE; PS00652; TNFR_M3FR_1; 3.
PROSITE; PS50050; TNFR_N3FR_2; 4.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1952 (Rel. 22, Last sequence update)
15-JUL 1999 (Rel. 38, Last annotation update)
TÜMÜR NEGROSIS FACTOR RECRITOR 2 PRECURSOR (TNF-P2) (P75).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.4%; Score 182.5; DB 1
32=1%; Pred No. 1 Re 08;
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TNFR-CYS 3.
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PS5113, P5789, STANDARD; P
P1-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequ
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45183 MW;
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Pfum, PF06020, TNFR_c6, 4.
SMART; SM00005; DRATH; 1.
SMART; SM00208; TNFR; 3.
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                                                                                      Phosphorylation; Signal
                                                                                                                                                                                                       147
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Best Local Similarity
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                                                                                                                "Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor."; Mol. Cell. Biol. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                     1- SIMILARITY: CONTAINS A LA-NGEK/INFR-IYPE CYSTEINE-KICH REGION.
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N-LINKED (GLCNAC, .,) (POTENTIAL).
452EAR339804D5563 (GRO64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUMOR NECROSIS FACTOR RECEPTOR 2.
necrosis factor receptors demonstrate one receptor is species
                                                                   MEDLINE-91246168; Pubmed 1645445,
Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.L.,
Copeland N.G., Jenkins N.A., Smith C.A.,
                                                                                                                                                                                                                                                                               Feldmann M., Chernajovsky Y.;
                                                                                                                                                                                                        Jacob C.O., Liu J.;
Submitted (TAN-1996) to the EMBL/GenBack/PDRT databases.
                                                                                                                                                                                                                                                                              Kissonerghis M., Fellowes K., Feldmann M., Chernajovsky Submitted (MAY-1995) in the Physician (PDRT databases FI FUNCTION: RECEPTOR FOR INF-ALPHA.

-1- FUNCTION: RECEPTOR FOR INF-ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
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                             Prog. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPOSITE; PS00652; INFP_NGFP_1: 2. PPOSITE; PS50050; INFP_NGFP_2: 3.
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InterPrc: IPP001369 TNFP--6
Pfam: PF00020; TNFR-c6; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: M60469; AAA39752.1; -.
                                                                                                                                                                                                                                                   SEQUENCE OF 1-22 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M59378; AAA40463.1;
EMBL; U39488; AAA85021.1;
EMBL; X87128; CAA60618.1;
                                                                                                                                                                           SHOURNCE OF 1-26 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00208; INFR; 4.
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HSSP; P19438; INCF.
                                                          SEQUENCE FROM N.A.
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"Myxoma virus expresses a serreted protein with homology to the tumor necrosis factor receptor qene lamily that contributes to viral virulence.";
Virulence.";
Virology 184:370-382(1991).
-i. FUNCTION: KINDS TO INF ALEMA AND HELA.
                                                                                                                                                                                                                                                                                                                         62 SKORKIMOGVEDSSOVENSKEVCOOKKRET 🗼 RETWOERLINGSELLAG 1VALG 117
                                                                                                                                                                                                                                                                                                                                                                                                              99 SSCTTD - QVETRACTKOGNEVÇACEAGRYCALKTH - - SAŞTRQETMRESKOBRAVASS 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses: dsDNA viruses, no RNA stage; Pexviridae; Chord-gexvirinae;
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01-APR/1994 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TUMOR NECROSIS FACIOR SCHOMLE RECEPTOR ERECHES (FREED IN 12).
41.7%; Pred No. 2.5c 08;
17c 20, Mishatches 76; inders
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INFR-CYS 3.
INFR-CYS 4.
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EMBL; A23729, CAA01688.1,
PIR; A40566; GUVZML.
HSSP; P19438; 11NR.
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ProDom; PD000771; INFR_c6,
Best Local Similarity 31,77 Matches 51, Conservative
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                                                                                                                                                                                                                                                      Opton C., Delange A.M., McFadden G.; "funnization and DNA sequence of the "funnization poxylibuses, genomic Ordanization and DNA sequence of the Lelomeric region of the Shope Libroma virus genome."; Virology 160:20-30(1987).
                                                                                                                                                                                         92 - ESQSCDKIRDRVCDCSAGNYCLLKGGGGGFFFAAFKCPAGYGVSGHIPFGDVLCTKCP-150
                                                                                                                                                                                                                                93 RHYWSENLFOCENCSLCLNG-LVHLSCOEKONTVCTCHAGFFLRENFCVSCSNCKKSLJEC 151
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                                                                          13 QNNSICCTKCHKGTYLYNDOPGPGQDTDCRECESGSFIASENHLRHGLSG-SKCRKEMGQ 71
                                                                                              Stochem Ricphys, Res. Commun. 176,335-312(1991).
-!- FUNCTION: BINDS TO TWE-ALPHA AND BETA, PROBABLY PREVENTS INF TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses: dsDNA viruses, no PNA stage: Pexviridae, Chordopexviridae;
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Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
McFadden G., Goodwin R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY, CONTAINS A LA NGFE/TNFR TYPE CYSTEINE-RICH REGION.
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15-JUL-1999 (Rel. 38, Last annotation update)
ITMOR NECROSIS FACTOR SOLURLE PECEPIOR PRECURSOR (PROTEIN T2).
19.1%; Score 179.5; DB 1; Longth 326; 27.4%; Pred. No. 2.6e.08.
                                      Indels
                                        67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                325 AA.
                                    19; Mismatches
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01-MAY-1992 (Rel. 22, Last sequ
15-JUE-1999 (Rel. 38, Last anno
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PROSITE; PSO0652: TNFF_NOFF_1.
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Pfam; PF00020; TNFR_c6; 2.
ProDom; PD000771; TNFR_c6; 1.
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                                    51; Conservative
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                  Similarity
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                                                                                                                                                                                                                                                                                                           152 TKLCLP 157
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Query Match
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modified and this statement is not removed. Usage by and for communerial
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1. SUBCEILLIAR LOCATION: TYPE I MICHARDE PROFIEIN.
                                                                                                                                                                                                                                                                                                                 30; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bartling B , Hoffmann J , Holtz J , Schelz R , Heusch G , Parmer D.; Ykpression of approxis associated genes in hibernating and stunned more action of a or "..."
                                                     TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: FONTAINS A LA-NAFE/THEF TYPE FYSTEINE-FICH REGION. SIMILARITY. CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
455. MCC-2101 (Rel. 40, Last annotation update)
(ARC-1 MATIGEN) (CDS)
(ARC-1 MATIGEN) (CDS)
TNFRSF6 OR APTI OR FAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Cianjata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                       . .) (POTENHIAL)
                                                                                                                                                                                      N-LINKED (GLCHAC. .) (POTENTIAL).
N-LINKED (GLCHAC. .) (POTENTIAL).
810530339198A71E CRC64;
                                                                                                                                                                                                                                                                            18.9%; Score 178: DH 1; Length 325; 29.6%; Pred. No. 3.46-08; Live 15, Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                       N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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                                                                   4 X TNFR-CYS.
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                                                                                    TNFR-CYS 1.
                                                                                                      TNFR-CYS 2.
                                                                                                                     TNFR-CYS 3.
TWFR-CYS 4.
                Siqual
                                POTENTIAL.
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TNFR_NGFR_2; 1.
                  Receptor; Glycoprotein; Repeat;
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PROSITE; PS50050;
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or send an email to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.3 FSPCPRCOH --- KPGGHGGGGGGGCKKKHANGTSPGGAPGCVPGSEGEDYTIKNHHSSKC 99
                                                                                                                                                                                                                                                                                                                                                                                             7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      1 DSVCPQGKYIHPQNNSICCIKCHKGTYLYNNCPGFGQDICGREGESG-SF1ASENHLRHC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa: Chordata; Craniata; Vertebrata: Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae: Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Padeke M.J., Misko T.F., Bsu C., Hersenberg L.A., Shoster E.M.; "Gene transfer and molecular cloning of the rat nerve growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metsis M., limmusk T., Allikmets R., Saarma M., Persson H.; "Regulatory elements and transcriptional regulation by testesterone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR0048B; Death.
Interpro; IPR0048B; Death.
Pfam; PP00531; doath: 1
Pfam; PP00531; doath: 1
Pfam; PP00531; DEATH: 1
SMART: SM00005; DEATH: 1.
SMART: SM020B; TNFR, 3.
PROSTITE: PS0050; TNFR_NGFR_2; 2.
PROSTITE: PS0050; TNFR_NGFR_2; 2.
PROSTITE: PS0017; DEATH_DOMAIN: 1.
Apoptosis; PS0017; DEATH_DOMAIN: 1.
Interprosis; PS0017; DEATH_DOMAIN: 1.
SIGNAL.
                                                                                                                                                                                                                                                                                                              5B8B036827558elb CRC54;
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N-LINKED (GLCNAC, . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                  Query Match 18.8%: Score 176.5; DH 1; Length 332; Best Local Similarity 29.1%; Pred. No. 4.7e.08;
                                                                                                                                                                                                                                                                                                                                                                                           65; Indels
                                                                                                                                                                                       FASL RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                POTENTIAL. CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                          3 X TNFR-CYS.
INFR-CYS 1.
INFR-CYS 2.
INFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                             18; Mismatches
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                                                                                                                                                                                                                                                                                           DEATH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93077038: PubMed-1446821;
                                     EMBL; AJ001202; CAA04596.1; ·.
                                                                                                                                                                                                                                                                                                                                 39555 MM
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                                                                                                                                                                                                                                                                                                                                                                                             37; Conservative
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164
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This SWISS-PRED COLLY is copyright. It is produced through a collaboration between the Saiss Institute of HiGhitormatics and the EMBI outstation - the European Biointormatics institutions as lond as its confert is in no way use by non-pioli institutions as lond as its confert is in no way involved and Lia statement is not tenored. Usage by and lot commercial coffice require a linear arteres. The lower of the commercial of send an email to increase beside.
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                                                                                         STRUCTURE BY NMR OF 334-418.
MEDLINE-97449145: PubMed-935'641;
Liophish E., Haq L.L., Orting G., Hancz G.E.;
"NMR STRUCTURE Of the death domain of the pTT neurotrophin receptor.";
EMBO J. 16:4939-5005(1997).
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i ibs ist selle grewib faciol receptor promoter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- FOMEN-A AND COUNCESTAILD AND TO THESPH BYLATED ON STRUME.
-1- SIMILARITY: CONTAINS A LA NOFR/THER TYPE CYSTEINE FISH REGION.
-1- SIMILARITY: CONTAINS I DEATH DOMAIN.
                                                                                                                                                                                                                                                                  11- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF, NT 3, AND NT 4.

5. SGESNIL: RGF RECEPTOR CAN FORM A HOROLIMER IIROGGH DISULFIDE BOND FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .) (F - HINITAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOW APPINITY NERVE GROWTH PACTOR
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Phosphorylation, Signal, 3D structure,
SIGNAL 1 29
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                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
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INFR-CYS 1.
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INFR CYS 3.
INFR CYS 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMEL, X61265, N.T.ANN/TATEL_CHS. PIR. A26431; A26431, DDB; INGR; 29-70L-97. (interPro; IPRO/G48H; Death. HiterPro; IPRO/G48H; DGST, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEATH
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Best Local Similarity 30,9
Matches 50, Conservative
F.3 P.115 J. A.154 J. 116
Gene 121:247-254(1992).
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15-UHL-1999 (Rel. 38, Last annotation update)
CDADL RECEPTOR PREPURSOR (R-CELL SHREAGE ANTIGEN CDAD) (RPSD) (CDMAD).
                                                                                                                                            63 SKOPKEMAQVETSS-OTVDPDTVOGOPKNQYPHYWSENLFQOFNOSLOLNGT-VHLSOQE 120
                                                                                                                                                                                                           88 TEC----LGLQSMSAPCVEADDAVCRC---AYGYYQDEETGHGEAGSVCEVGSGLVFSQQD 141
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                                    4 CPQGKYTHPQNNSTGCTKCHKGTVLYNPCPGPGGGTECTECTECT-ESGSFTASENHLRHCLSC 62
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!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPF CYSTEINE-PICH PEGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enkaryota, Metazoa, Chordata, Cranjata, Verfebrata, Euteleostumi,
Mammulia: Eutheria: Rodentia: Sciuroquathi: Muridae: Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92105763; PubMed-1370315;
Torres R.M., Clark E.A.;
"Diliverential increase of an alternatively polyadenylated mRNA
species of morine C140 upon H lymphocyte activation.";
J. Immanol. 148:620-626(1992).
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MEDLINE-93094586; Pubmed-1281194;
Grimhidi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
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                                                                                                                                                                                                                                                                                     121 KONTVC-TCHAGFFLRE----NECVSCSNCKKSLECTKLCLP 157
                                                                                                                                                                                                                                                                                                                                                       142 KONTVCEECPEGTYSDEANHVDPCLPCTVCEDTERQLRECTP 183
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EMBL: M94126; AAA37404.1; -..
EMBL: M94129; AAA37404.1; JOINED.
EMBL: M94128; AAA37404.1; JOINED.
EMBL: M94127; AAA37404.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | H; A4000.0.
| ISSP: P25942, | ICPF.
| AGD: MGI: 88476; | Thirsi5.
| InterPro; | IPR001156; | ThFR_C6.
| The Through | Throug
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P27512.
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REVISIONS.
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Browning J.L., Ware C.F.,
"Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-HETA, POSSIBLE FUNCTION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 CPQGKYIHPQNNSICCIKCHKGIYLYNDCPGPGQDIDCKECESGSFTASENHLKHCLSCS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 CSDKQYLH---DQQCCDLQQPGSRLTSHCTAL-EKTOCHPCDSGEFSAQWNKETRCHQHR 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Veilebrata; Euteleostomi;
Mammalia; Eutheria, Rodentia; Sciuroquathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                       .) (POTENTIAL)
Receptor: B-cell; Glycoprotein; Transmembrane; Repeat; Sianal
SIGNAL 1 19 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.8%; Score 167 5; DB 1; Length 289;
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                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                             C791CB6D2FEA574E CRC64;
                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 2.3e-07;
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01-OCT-1996 (Rel. 34, Last sequence update)
01-WV-1997 (Rel. 35, Last annotation update)
LYMPHOTOXIN-HETA RECEPTOR PHECURSOR.
                                                              CD401, RECEPTOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23; Mismatches
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                                                                                                                                                                                    4 X INFR-CYS.
                                                                                                                                                                                                             TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                    TNFR-CYS 4.
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                                                                                                                         POTENTIAL.
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STRAIN-(VB; IISSUE-Lung;
MEDLINE-96072804; PubMed-7594541;
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J. Immunol. 155:5280-5288(1995).
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289 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           LYMPHOTOXIN-BETA RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                         Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL). 4 X INFR-CYS.
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
or send an email to license dish-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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PROSITE: PSSG050; TNFR_NGFR_2; 3.
                                                                                                                                      MESSP: P25642: 1CDF.
MGD: MGI:104875: LLbr.
InterPro: IPR001368: TNFR_c6.
Promom: PF00020: TNFR_c6: 3.
Promom: PP000271: TNFR_c6: 1.
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                                                 EMBL; U29173; AAA68964.1;
EMBL; L38423; AAB00846.1;
EMBL; U30798; AAAB1344.1;
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179
415 AA;
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Search completed; April 24, 2552, 13.49:10 Job time: 672 sec

